

CRF Errors Corrected by the STIC System Branch

Batch 1641
10/22/98 #9

Serial Number: 08/908,453

CRF Processing Date: 10/22/98
 Edited by: _____
 Verified by: JW (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☒ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☒ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/908,453DATE: 10/22/98
TIME: 09:36:26

INPUT SET: S29199.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: Ruvkun, Gary
6 Morris, Jason
7 Tissenbaum, Heidi
8
9 (ii) TITLE OF THE INVENTION: AGE-1 POLYPEPTIDES AND RELATED
10 MOLECULES AND METHODS
11
12 (iii) NUMBER OF SEQUENCES: 14
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Clark & Elbing LLP
16 (B) STREET: 176 Federal Street
17 (C) CITY: Boston
18 (D) STATE: MA
19 (E) COUNTRY: USA
20 (F) ZIP: 02110
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Diskette
24 (B) COMPUTER: IBM Compatible
25 (C) OPERATING SYSTEM: DOS
26 (D) SOFTWARE: FastSEQ for Windows Version 2.0
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER:
30 (B) FILING DATE:
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: US97/13914
35 (B) FILING DATE: 07-AUG-1997
36
37 (A) APPLICATION NUMBER: 60/023,382
38 (B) FILING DATE: 07-AUG-1996
39
40
41 (viii) ATTORNEY/AGENT INFORMATION:
42 (A) NAME: Elbing, Karen L
43 (B) REGISTRATION NUMBER: 35,238
44 (C) REFERENCE/DOCKET NUMBER: 08472/704W02
45
46 (ix) TELECOMMUNICATION INFORMATION:

RAW SEQUENCE LISTING

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DATE: 10/22/98
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INPUT SET: S29199.raw

47 (A) TELEPHONE: 617-428-0200
48 (B) TELEFAX: 617-428-7045
49 (C) TELEX:
50
51

52 (2) INFORMATION FOR SEQ ID NO:1:
53

54 (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 1146 amino acids
56 (B) TYPE: amino acid
57 (C) STRANDEDNESS: unknown
58 (D) TOPOLOGY: linear
59

60 (ii) MOLECULE TYPE: protein
61

62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63

64	Met	His	Val	Asn	Ile	Leu	His	Pro	Gln	Leu	Gln	Thr	Met	Val	Glu	Gln
65	1				5					10					15	
66	Trp	Gln	Met	Arg	Glu	Arg	Pro	Ser	Leu	Glu	Thr	Glu	Asn	Gly	Lys	Gly
67				20					25					30		
68	Ser	Leu	Leu	Leu	Glu	Asn	Glu	Gly	Val	Ala	Asp	Ile	Ile	Thr	Met	Cys
69			35					40				45				
70	Pro	Phe	Gly	Glu	Val	Ile	Ser	Val	Val	Phe	Pro	Trp	Phe	Leu	Ala	Asn
71		50					55					60				
72	Val	Arg	Thr	Ser	Leu	Glu	Ile	Lys	Leu	Ser	Asp	Phe	Lys	His	Gln	Leu
73		65				70					75				80	
74	Phe	Glu	Leu	Ile	Ala	Pro	Met	Lys	Trp	Gly	Thr	Tyr	Ser	Val	Lys	Pro
75				85						90					95	
76	Gln	Asp	Tyr	Val	Phe	Arg	Gln	Leu	Asn	Asn	Phe	Gly	Glu	Ile	Glu	Val
77			100						105					110		
78	Ile	Phe	Asn	Asp	Asp	Gln	Pro	Leu	Ser	Lys	Leu	Glu	Leu	His	Gly	Thr
79			115					120					125			
80	Phe	Pro	Met	Leu	Phe	Leu	Tyr	Gln	Pro	Asp	Gly	Ile	Asn	Arg	Asp	Lys
81		130					135					140				
82	Glu	Leu	Met	Ser	Asp	Ile	Ser	His	Cys	Leu	Gly	Tyr	Ser	Leu	Asp	Lys
83		145				150					155				160	
84	Leu	Glu	Glu	Ser	Leu	Asp	Glu	Glu	Leu	Arg	Gln	Phe	Arg	Ala	Ser	Leu
85				165						170					175	
86	Trp	Ala	Arg	Thr	Lys	Lys	Thr	Cys	Leu	Thr	Arg	Gly	Leu	Glu	Gly	Thr
87			180						185					190		
88	Ser	His	Tyr	Ala	Phe	Pro	Glu	Glu	Gln	Tyr	Leu	Cys	Val	Gly	Glu	Ser
89			195					200					205			
90	Cys	Pro	Lys	Asp	Leu	Glu	Ser	Lys	Val	Lys	Ala	Ala	Lys	Leu	Ser	Tyr
91		210					215					220				
92	Gln	Met	Phe	Trp	Arg	Lys	Arg	Lys	Ala	Glu	Ile	Asn	Gly	Val	Cys	Glu
93		225				230					235				240	
94	Lys	Met	Met	Lys	Ile	Gln	Ile	Glu	Phe	Asn	Pro	Asn	Glu	Thr	Pro	Lys
95				245					250						255	
96	Ser	Leu	Leu	His	Thr	Phe	Leu	Tyr	Glu	Met	Arg	Lys	Leu	Asp	Val	Tyr
97			260						265					270		
98	Asp	Thr	Asp	Asp	Pro	Ala	Asp	Glu	Gly	Trp	Phe	Leu	Gln	Leu	Ala	Gly
99			275					280					285			

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100	Arg	Thr	Thr	Phe	Val	Thr	Asn	Pro	Asp	Val	Lys	Leu	Thr	Ser	Tyr	Asp
101		290					295					300				
102	Gly	Val	Arg	Ser	Glu	Leu	Glu	Ser	Tyr	Arg	Cys	Pro	Gly	Phe	Val	Val
103		305				310					315					320
104	Arg	Arg	Gln	Ser	Leu	Val	Leu	Lys	Asp	Tyr	Cys	Arg	Pro	Lys	Pro	Leu
105					325					330						335
106	Tyr	Glu	Pro	His	Tyr	Val	Arg	Ala	His	Glu	Arg	Lys	Leu	Ala	Leu	Asp
107					340					345						350
108	Val	Leu	Ser	Val	Ser	Ile	Asp	Ser	Thr	Pro	Lys	Gln	Ser	Lys	Asn	Ser
109			355					360					365			
110	Asp	Met	Val	Met	Thr	Asp	Phe	Arg	Pro	Thr	Ala	Ser	Leu	Lys	Gln	Val
111		370					375						380			
112	Ser	Leu	Trp	Asp	Leu	Asp	Ala	Asn	Leu	Met	Ile	Arg	Pro	Val	Asn	Ile
113		385				390					395					400
114	Ser	Gly	Phe	Asp	Phe	Pro	Ala	Asp	Val	Asp	Met	Tyr	Val	Arg	Ile	Glu
115					405					410						415
116	Phe	Ser	Val	Tyr	Val	Gly	Thr	Leu	Thr	Leu	Ala	Ser	Lys	Ser	Thr	Thr
117					420					425					430	
118	Lys	Val	Asn	Ala	Gln	Phe	Ala	Lys	Trp	Asn	Lys	Glu	Met	Tyr	Thr	Phe
119			435					440					445			
120	Asp	Leu	Tyr	Met	Lys	Asp	Met	Pro	Pro	Ser	Ala	Val	Leu	Ser	Ile	Arg
121		450					455					460				
122	Val	Leu	Tyr	Gly	Lys	Val	Lys	Leu	Lys	Ser	Glu	Glu	Phe	Glu	Val	Gly
123		465				470					475					480
124	Trp	Val	Asn	Met	Ser	Leu	Thr	Asp	Trp	Arg	Asp	Glu	Leu	Arg	Gln	Gly
125					485					490						495
126	Gln	Phe	Leu	Phe	His	Leu	Trp	Ala	Pro	Glu	Pro	Thr	Ala	Asn	Arg	Ser
127					500					505					510	
128	Arg	Ile	Gly	Glu	Asn	Gly	Ala	Arg	Ile	Gly	Thr	Asn	Ala	Ala	Val	Thr
129			515					520					525			
130	Ile	Glu	Ile	Ser	Ser	Tyr	Gly	Gly	Arg	Val	Arg	Met	Pro	Ser	Gln	Gly
131		530					535					540				
132	Gln	Tyr	Thr	Tyr	Leu	Val	Lys	His	Arg	Ser	Thr	Trp	Thr	Glu	Thr	Leu
133		545				550					555					560
134	Asn	Ile	Met	Gly	Asp	Asp	Tyr	Glu	Ser	Cys	Ile	Arg	Asp	Pro	Gly	Tyr
135					565					570					575	
136	Lys	Lys	Leu	Gln	Met	Leu	Val	Lys	Lys	His	Glu	Ser	Gly	Ile	Val	Leu
137					580					585					590	
138	Glu	Glu	Asp	Glu	Gln	Arg	His	Val	Trp	Met	Trp	Arg	Arg	Tyr	Ile	Gln
139			595					600					605			
140	Lys	Gln	Glu	Pro	Asp	Leu	Leu	Ile	Val	Leu	Ser	Glu	Leu	Ala	Phe	Val
141		610					615					620				
142	Trp	Thr	Asp	Arg	Glu	Asn	Phe	Ser	Glu	Leu	Tyr	Val	Met	Leu	Glu	Lys
143		625				630					635					640
144	Trp	Lys	Pro	Pro	Ser	Val	Ala	Ala	Ala	Leu	Thr	Leu	Leu	Gly	Lys	Arg
145					645					650					655	
146	Cys	Thr	Asp	Arg	Val	Ile	Arg	Lys	Phe	Ala	Val	Glu	Lys	Leu	Asn	Glu
147					660				665						670	
148	Gln	Leu	Ser	Pro	Val	Thr	Phe	His	Leu	Phe	Ile	Leu	Pro	Leu	Ile	Gln
149			675					680					685			
150	Ala	Leu	Lys	Tyr	Glu	Pro	Arg	Ala	Gln	Ser	Glu	Val	Gly	Met	Met	Leu
151		690					695					700				
152	Leu	Thr	Arg	Ala	Leu	Cys	Asp	Tyr	Arg	Ile	Gly	His	Arg	Leu	Phe	Trp

RAW SEQUENCE LISTING PATENT APPLICATION US/08/908,453

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153	705				710				715				720			
154	Leu	Leu	Arg	Ala	Glu	Ile	Ala	Arg	Leu	Arg	Asp	Cys	Asp	Leu	Lys	Ser
155					725				730					735		
156	Glu	Glu	Tyr	Arg	Arg	Ile	Ser	Leu	Leu	Met	Glu	Ala	Tyr	Leu	Arg	Gly
157				740					745					750		
158	Asn	Glu	Glu	His	Ile	Lys	Ile	Ile	Thr	Arg	Gln	Val	Asp	Met	Val	Asp
159				755					760				765			
160	Glu	Leu	Thr	Arg	Ile	Ser	Thr	Leu	Val	Lys	Gly	Met	Pro	Lys	Asp	Val
161		770					775					780				
162	Ala	Thr	Met	Lys	Leu	Arg	Asp	Glu	Leu	Arg	Ser	Ile	Ser	His	Lys	Met
163	785					790					795					800
164	Glu	Asn	Met	Asp	Ser	Pro	Leu	Asp	Pro	Val	Tyr	Lys	Leu	Gly	Glu	Met
165				805					810					815		
166	Ile	Ile	Asp	Lys	Ala	Ile	Val	Leu	Gly	Ser	Ala	Lys	Arg	Pro	Leu	Met
167			820						825					830		
168	Leu	His	Trp	Lys	Asn	Lys	Asn	Pro	Lys	Ser	Asp	Leu	His	Leu	Pro	Phe
169			835					840					845			
170	Cys	Ala	Met	Ile	Phe	Lys	Asn	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu
171		850					855				860					
172	Val	Leu	Gln	Val	Leu	Glu	Val	Met	Asp	Asn	Ile	Trp	Lys	Ala	Ala	Asn
173	865					870					875					880
174	Ile	Asp	Cys	Cys	Leu	Asn	Pro	Tyr	Ala	Val	Leu	Pro	Met	Gly	Glu	Met
175				885					890					895		
176	Ile	Gly	Ile	Ile	Glu	Val	Val	Pro	Asn	Cys	Lys	Thr	Ile	Phe	Glu	Ile
177			900					905					910			
178	Gln	Val	Gly	Thr	Gly	Phe	Met	Asn	Thr	Ala	Val	Arg	Ser	Ile	Asp	Pro
179			915					920					925			
180	Ser	Phe	Met	Asn	Lys	Trp	Ile	Arg	Lys	Gln	Cys	Gly	Ile	Glu	Asp	Glu
181		930					935					940				
182	Lys	Lys	Lys	Ser	Lys	Lys	Asp	Ser	Thr	Lys	Asn	Pro	Ile	Glu	Lys	Lys
183	945					950					955					960
184	Ile	Asp	Asn	Thr	Gln	Ala	Met	Lys	Lys	Tyr	Phe	Glu	Ser	Val	Asp	Arg
185				965					970					975		
186	Phe	Leu	Tyr	Ser	Cys	Val	Gly	Tyr	Ser	Val	Ala	Thr	Tyr	Ile	Met	Gly
187			980					985					990			
188	Ile	Lys	Asp	Arg	His	Ser	Asp	Asn	Leu	Met	Leu	Thr	Glu	Asp	Gly	Lys
189			995				1000					1005				
190	Tyr	Val	His	Ile	Asp	Phe	Gly	His	Ile	Leu	Gly	His	Gly	Lys	Thr	Lys
191		1010					1015				1020					
192	Leu	Gly	Ile	Gln	Arg	Asp	Arg	Gln	Pro	Phe	Ile	Leu	Thr	Glu	His	Phe
193	025				1030						1035					1040
194	Met	Thr	Val	Ile	Arg	Ser	Gly	Lys	Ser	Val	Asp	Gly	Asn	Ser	His	Glu
195				1045					1050					1055		
196	Leu	Gln	Lys	Phe	Lys	Thr	Leu	Cys	Val	Glu	Ala	Tyr	Glu	Val	Met	Trp
197			1060					1065					1070			
198	Asn	Asn	Arg	Asp	Leu	Phe	Val	Ser	Leu	Phe	Thr	Leu	Met	Leu	Gly	Met
199			1075				1080					1085				
200	Glu	Leu	Pro	Glu	Leu	Ser	Thr	Lys	Ala	Asp	Leu	Asp	His	Leu	Lys	Lys
201		1090					1095				1100					
202	Thr	Leu	Phe	Cys	Asn	Gly	Glu	Ser	Lys	Glu	Glu	Ala	Arg	Lys	Phe	Phe
203	105				1110						1115					1120
204	Ala	Gly	Ile	Tyr	Glu	Ala	Phe	Asn	Gly	Ser	Trp	Ser	Thr	Lys	Thr	
205				1125					1130					1135		

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/908,453DATE: 10/22/98
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INPUT SET: S29199.raw

206 Asn Trp Leu Phe His Ala Val Lys His Tyr
207 1140 1145
208209 (2) INFORMATION FOR SEQ ID NO:2:
210

211 (i) SEQUENCE CHARACTERISTICS:

212 (A) LENGTH: 3504 base pairs

213 (B) TYPE: nucleic acid

214 (C) STRANDEDNESS: double

215 (D) TOPOLOGY: linear
216217 (ii) MOLECULE TYPE: cDNA
218219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
220

221	CGGAAGCCAT	GGAGCTCGAG	ATCTGATTGC	TGGACACGGA	CGGAACTCCG	ACGTATCTCG	60
222	CAGATGCATG	TTAACATTTT	ACATCCACAA	CTGCAAACGA	TGGTCGAGCA	GTGGCAAAATG	120
223	CGAGAACGCC	CATCGCTGGA	GACCGAGAAT	GGCAAAGGAT	CGCTGCTCCT	GGAAAAATGAA	180
224	GGTGTGCGCAG	ATATCATCAC	TATGTGTCCA	TTCGGAGAAG	TTATTAGTGT	AGTATTTCCG	240
225	TGGTTTCTTG	CAAAATGTGCG	AACATCGCTA	GAAATCAAGC	TATCAGATTT	CAAAACATCAA	300
226	CTTTTCGAAAT	TGATTGCTCC	GATGAAAGTG	GGAACATATT	CCGTAAAAGCC	ACAGGATTAT	360
227	GTGTTTCAGAC	AGTTGAATAA	TTTCGGCGAA	ATTGAAAGTTA	TATTTAACGA	CGATCAACCC	420
228	CTGTGCGAAAT	TAGAGCTCCA	CGGCACTTTC	CCAATGCTTT	TTCTCTACCA	ACCTGATGGA	480
229	ATAAACAGGG	ATAAAGAATT	AATGAGTGAT	ATAAGTCATT	GTCTAGGATA	CTCACTGGAT	540
230	AAACTGGAAG	AGAGCCTCGA	TGAGGAACTC	CGTCAATTTT	GTGCTTCTCT	CTGGGCTCGT	600
231	ACGAAGAAAA	CGTGCTTGAC	ACGTGGACTT	GAGGGTACCA	GTCACACGCG	GTCCCCCGAA	660
232	GAACAGTACT	TGTGTGTTGG	TGAATCGTGC	CCGAAAAGATT	TGGAAATCAA	AGTCAAAGGCT	720
233	GCCAAGCTGA	GTTATCAGAT	GTTTGTGGAGA	AAACGTAAAG	CGGAAATCAA	TGGAGTTTGC	780
234	GAGAAAAATGA	TGAAGATTCA	AATTGAATTC	AATCCGAACG	AAACTCCGAA	ATCTCTGCTT	840
235	CACACGTTTC	TCTACGAAAT	GCGAAAATTG	GATGTATACG	ATACCGATGA	TCCTGCAGAT	900
236	GAAGGATGGT	TTCTTCAATT	GGCTGGACGT	ACCACGTTTG	TTACAAATCC	AGATGTCAAA	960
237	CTTACGTCTT	ATGATGGTGT	CCGTTTCGGA	CTGGAAGGCT	ATCGATGCCC	TGGATTTCGTT	1020
238	GTTCCGCCGAC	AATCACTAGT	CCTCAAAGAC	TATTGTGCGC	CAAAACCACT	CTACGAACCA	1080
239	CATTATGTGA	GAGCACACGA	ACGAAAACCT	GCTCTAGACG	TGCTCAGCGT	GTCTATAGAT	1140
240	AGCACACCAA	AACAGAGCAA	GAACAGTGAC	ATGGTTATGA	CTGATTTTCG	TCCGACAGCT	1200
241	TCACTCAAAC	AAGTTTCACT	TTGGGACCTT	GACGCGAATC	TTATGATACG	GCCTGTGAAT	1260
242	ATTTCTGGAT	TCGATTTCCC	GGCCGACGTG	GATATGTACG	TTCGAATCGA	ATTCAAGTGT	1320
243	TATGTGGGGA	CACTGACGCT	GGCATCAAAA	TCTACAACAA	AAGTGAATGC	TCAATTTGCA	1380
244	AAATGGAATA	AGGAAATGTA	CACTTTTGTG	CTATACATGA	AGGATATGCC	ACCATCTGCA	1440
245	GTAATCAGCA	TTCTGTGTTT	GTACGGAAAA	GTGAAATTAA	AAAGTGAAGA	ATTGCAAGTT	1500
246	GGTTGGGTAA	ATATGTCCCT	AACCGATTGG	AGAGATGAAC	TACGACAAGG	ACAATTTTAA	1560
247	TTCCATCTGT	GGGCTCCTGA	ACCGACTGCC	AATCGTAGTA	GGATCCGAGA	AAATGGAGCA	1620
248	AGGATAGGCA	CCAACGCAGC	GGTTACAATT	GAAATCTCAA	GTTATGGTGG	TAGAGTTTCGA	1680
249	ATGCCGAGTC	AAGGACAATA	CACATATCTC	GTCAAGCACC	GAAGTACTTG	GACGGAAACT	1740
250	TTGAATATTA	TGGGTGATGA	CTATGAGTCG	TGTATCAGAG	ATCCAGGATA	TAAGAAGCTT	1800
251	CAGATGCTTG	TCAAGAAGCA	TGAATCTGGA	ATTGTATTAG	AGGAAGATGA	ACAACGTCAT	1860
252	GTCTGGATGT	GGAGGAGATA	CATTCAAAAAG	CAGGAGCCTG	ATTTGCTCAT	TGTGCTCTCC	1920
253	GAACCTCGCAT	TTGTGTGGAC	TGATCGTGAG	AACTTTTCCTG	AGCTCTATGT	GATGCTTGAA	1980
254	AAATGGAAAC	CGCCGAGTGT	GGCAGCCGCG	TTGACTTTTGC	TTGGAAAAACG	TTGCACGGAT	2040
255	CGTGTGATTC	GAAAGTTTGC	AGTGGAGAAG	TTGAATGAGC	AGCTGAGCCC	GGTCACATTG	2100
256	CATCTTTTCA	TATTGCTCTC	TATACAGGCG	TTGAAAGTACG	AACCGCGTGC	TCAATCGGAA	2160
257	GTTGGAATGA	TGCTCTTGAC	TAGAGCTCTC	TGCGATTATC	GAATTGGACA	TGCACTTTTC	2220
258	TGGCTGCTCC	GTGCAGAGAT	TGCTCGTTTG	AGAGATTGTG	ATCTGAAAAG	TGAAGAATAT	2280

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